Fig. 1.

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TTCTATTGCATCAACCATATCATACCTAGACA/TATGCTTTTGTCTTCATTGGCTCAAG
CTACGGAGATTCACAGGTACTTTTAACTGTTGAGTGCATCTTGGTGCAATAAGTTGGTTT
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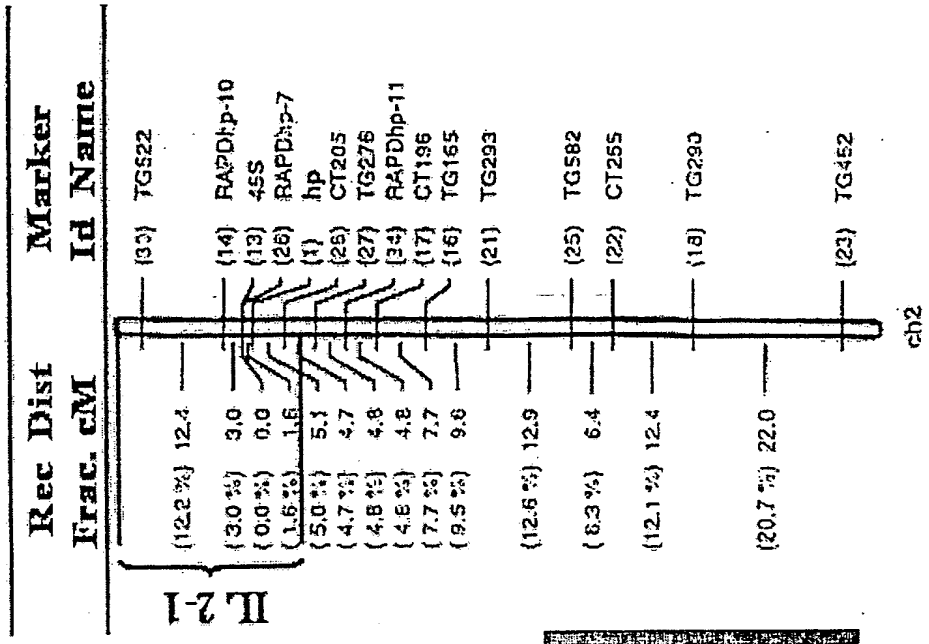
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Frac. cM
Marker
Id Name
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(3.0 %) 3.0
(0.0 %) 0.0
(1.6 %) 1.6
(5.0 %) 5.1
(4.7 %) 4.7
(4.8 %) 4.8
(4.6 %) 4.8
(7.7 %) 7.7
(9.5 %) 9.6
(12.6 %) 12.9
(6.3 %) 6.4
(12.1 %) 12.4
(20.7 %) 22.0
(33) TG522
(14) RAPDhp-10
(13) 45S
(26) RAPDhp-7
(1) hp
(25) CT205
(27) TG276
(34) RAPDhp-11
(17) CT196
(16) TG165
(21) TG293
(25) TG582
(22) CT255
(18) TG290
(23) TG452
ch2

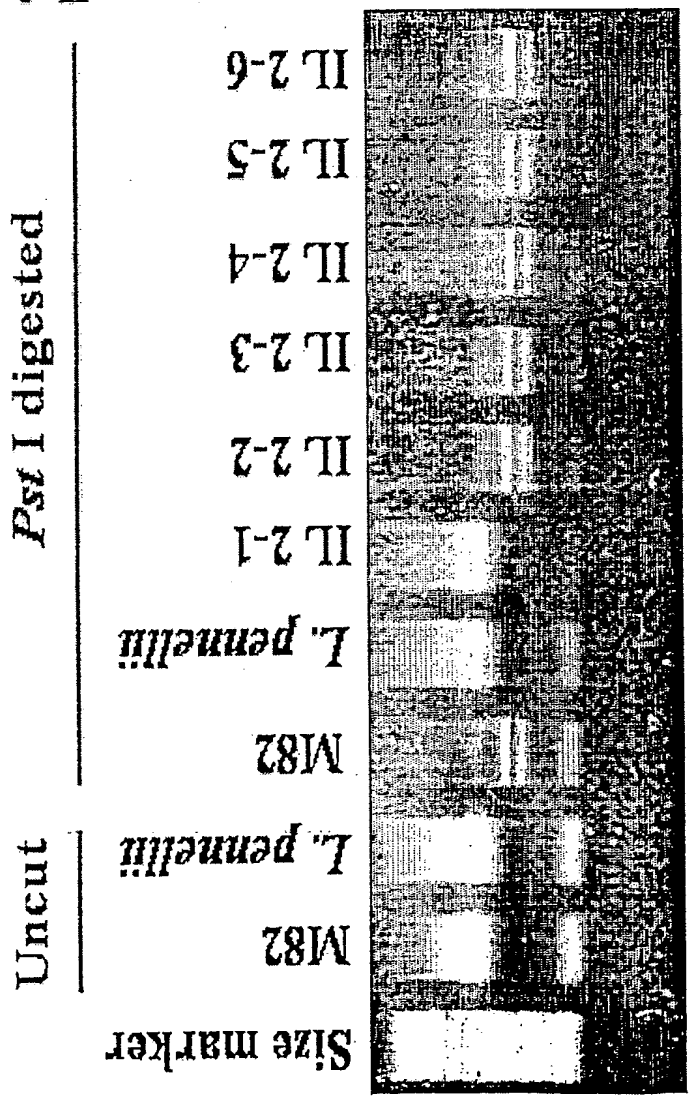
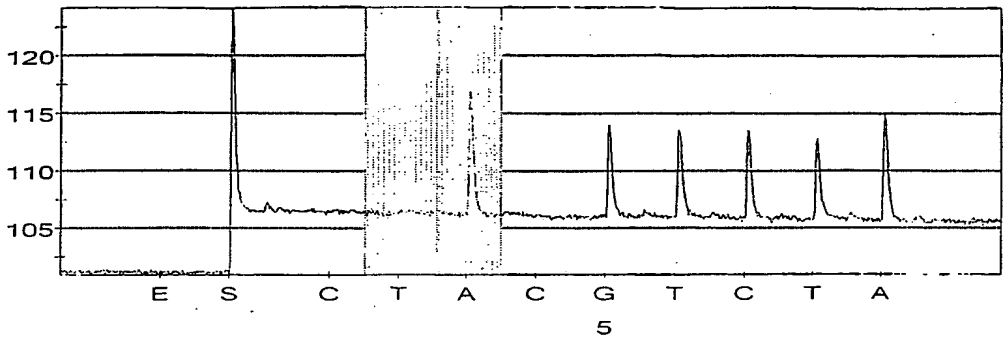

Size marker
Uncut
M82
L. pennellii
PstI digested
M82
L. pennellii
IL 2-1
IL 2-2
IL 2-3
IL 2-4
IL 2-5
IL 2-6

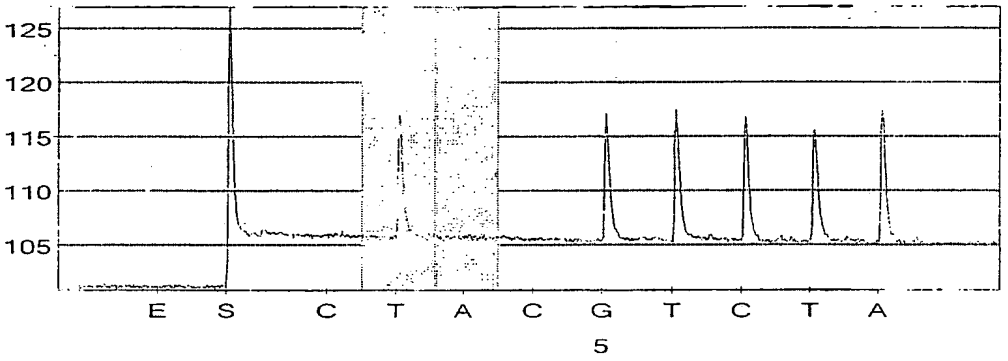
Fig. 2

Fig. 3

a. *hp-1/hp-1*



b. +/+



c. *hp-1/+*

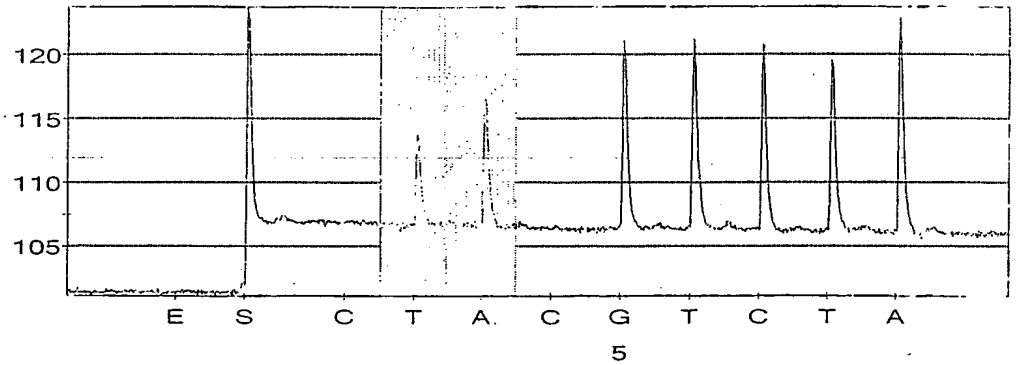


Fig. 4

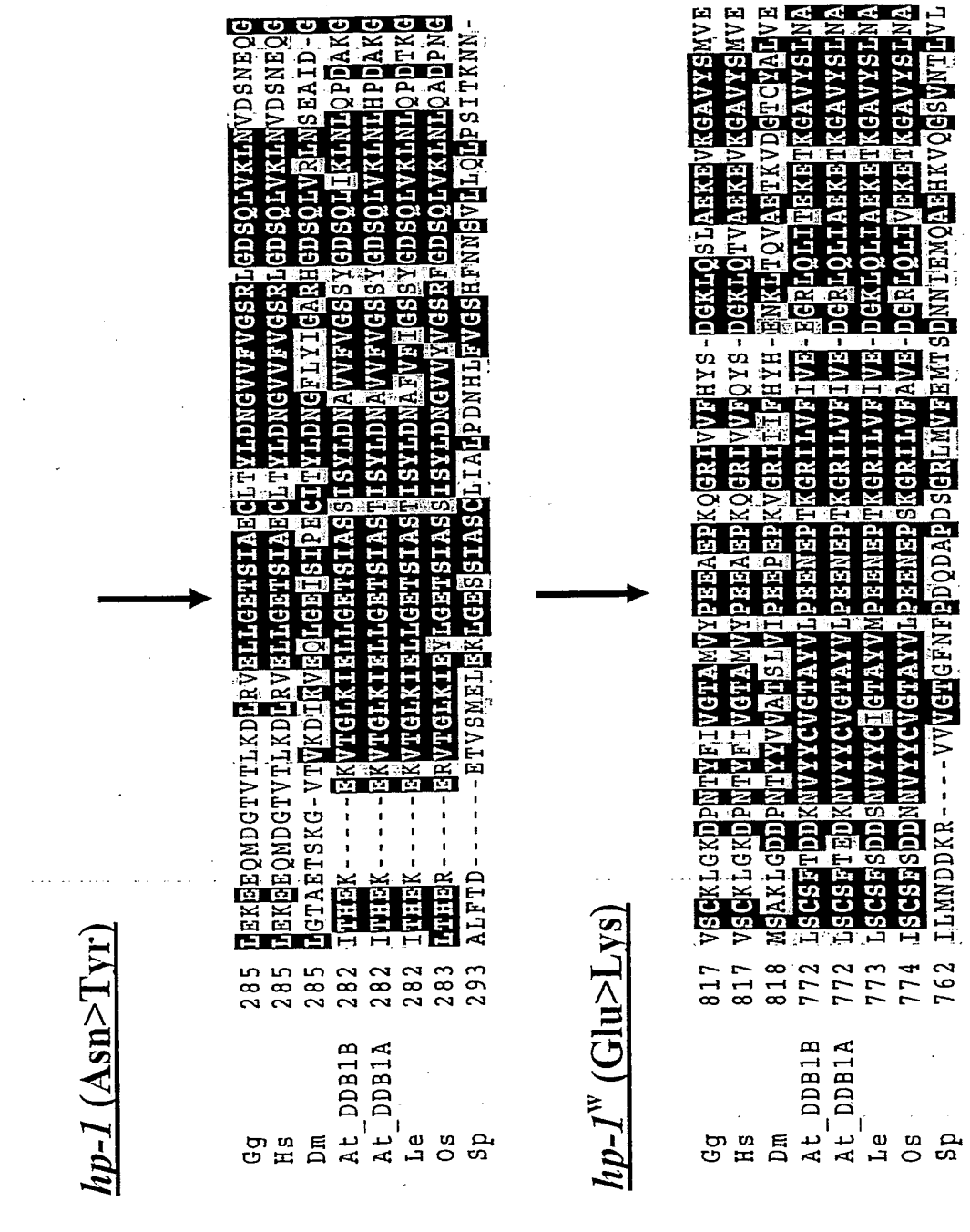


Fig. 5

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 161 TAGATGTGCCAATATATGGGAGGATCGCGACACTTGAGCTTTTTCGTCCTCACGGTGAAACACAAGATCTTCTCTTCATC
 241 GCAACAGAGCGATATAAATTCTGTGTCCTTCAATGGGATACTGAGGCATCTGAAGTTATCACAAGAGCAATGGGAGATGT
 321 GTCAGACCGAATAGGCCGTCCCACAGATAATGGTCAGATTGGTATAATTGATCCAGATTGCAGATTGATCGGGCTACATC
 401 TTTATGATGGACTATTTAAGGTTATTCCATTTGATAACAAAGGCCAACTGAAGGAAGCTTTTAACATCAGGCTCGAGGAG
 481 CTTCAAGTTTTAGATATTAAATTCTTGTATGGTTGCCCAAAGCCTACAATTGTTGTTCTATATCAGGATAACAAGGATGC
 561 CCGGCATGTCAAAACATATGAGGTGTCCTTGAAAGACAAAGATTTTATTGAAGGGCCATGGGCTCAAAATAATCTTGATA
 641 ATGGAGCTTCTTTGCTAATACCAGTACCTCCACCACTGTGTGGTGTATTGATTATTGGAGAAGAAACCATCGTTTATTGC
 721 AGCGCTTCAGCTTTTAAGGCTATCCCAATTAGACCTTCTATCACAAGAGCATATGGGCGGGTTGATGCTGATGGTTCTCG
 801 ATATTTGCTTGGGGATCATAATGGGCTTCTTCACCTACTTGTAATCACTCATGAGAAGGAGAAAGTTACCGGACTCAAAA
 881 TTGAGCTACTGGGGGAAACTTCTATTGCATCAACCATATCATACCTAGACAATGCTTTTGTCTTCATTGGCTCAAGCTAC
 961 GGAGATTCACAGCTTGTAAAGCTCAATCTCCAGCCTGACACCAAAGGTTCTTATGTGGAAGTTCTAGAGAGATATGTCAA
1041 TTTAGGACCTATTGTGGACTTCTGTGTTGTTGATCTGGAAAGGCAAGGTCAAGGTCAGGTTGTAACTTGCTCTGGAGCCT
1121 ATAAGGATGGATCACTTCGTATTGTTCGAAATGGAATTGGCATAAATGAACAGGCGTCTGTGGAACTACAAGGGATCAAA
1201 GGAATGTGGTCTCTTAGATCTGCTACTGATGATCCATATGACACATTCTTGGTTGTTAGCTTCATTAGTGAGACACGCGT
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1361 ATGATGCTGTATACAACCAGCTTGTTCAGGTTACTTCAAATTCTGTTAGATTGGTCAGTTCTACCTCTAGAGATCTGAAA
1441 AACGAGTGGTTTGCCCCAGTCGGCTACTCGGTCAATGTTGCAACTGCTAATGCCACTCAGGTACTATTGGCTACTGGGGG
1521 TGGCCATCTGGTATACCTAGAAATTGGTGATGGGGTGTTGAATGAAGTAAAATATGCCAAGTTGGATTATGATATCTCGT
1601 GCCTGGACATAAATCCAATTGGTGAAAATCCGAACTACAGTAACATTGCAGCAGTTGGAATGTGGACAGACATAAGTGTC
1681 AGGATATATTCACTTCCTGACTTGAATCTCATTACAAAGGAACAGCTAGGAGGGGAGATAATTCCTCGTTCTGTTCTGAT
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2081 CAATTGGCACTATTGATGAAATTCAAAAGCTTCACATTCGTTCAATACCCCTTGGGGAGCATGCACGTCGCATCAGCCAT
2161 CAAGAGCAGACCCGGACATTTGCTCTATGCAGTGTGAAGTATACTCAGTCAAATGCAGATGATCCTGAAATGCATTTTGT
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Fig. 6

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   1 MSVWNYVVTAHKPTNVTHSCVGNFTGPQELNLIIAKCTRIEIHLLTPQGLQPMLDVPIYGRIATLELFRPHGETQDLLFI
  81 ATERYKFCVLQWDTEASEVITRAMGDVSDRIGRPTDNGQIGIIDPDCRLIGLHLYDGLFKVIPFDNKGQLKEAFNIRLEE
 161 LQVLDIKFLYGCPKPTIVVLYQDNKDARHVKTYEVSLKDKDFIEGPWAQNNLDNGASLLIPVPPPLCGVLIIGEETIVYC
 241 SASAFKAIPIRPSITRAYGRVDADGSRYLLGDHNGLLHLLVITHEKEKVTGLKIELLGETSIASTISYLDNAFVFIGSSY
 321 GDSQLVKLNLQPDTKGSYVEVLERYVNLGPIVDFCVVDLERQGQGQVVTCSGAYKDGSLRIVRNGIGINEQASVELQGIK
 401 GMWSLRSATDDPYDTFLVVSFISETRVLAMNLEDELEETEIEGFNSQVQTLFCHDAVYNQLVQVTSNSVRLVSSTSRDLK
 481 NEWFAPVGYSVNVATANATQVLLATGGGHLVYLEIGDGVLNEVKYAKLDYDISCLDINPIGENPNYSNIAAVGMWTDISV
 561 RIYSLPDLNLITKEQLGGEIIPRSVLMCSFEGISYLLCALGDGHLLNFVLSMSTGELTDRKKVSLGTQPITLRTFSSKDT
 641 THVFAASDRPTVIYSSNKKLLYSNVNLKEVSHMCPFNVAAFPDSLAIAKEGELTIGTIDEIQKLHIRSIPLGEHARRISH
 721 QEQTRTFALCSVKYTQSNADDPEMHFVRLLDDQTFEFISTYPLDQFEYGCSILSCSFSDDSNVYYCIGTAYVMPEENEPT
 801 KGRILVFIVEDGKLQLIAEKETKGAVYSLNAFNGKLLAAINQKIQLYKWASREDGGSRELQTECGHHGHILALYVQTRGD
 881 FIVVGDLMKSISLLIFKHEEGAIEERARDYNANWMSAVEILDDDIYLGAENNFNLFTVRKNSEGATDEERSRLEVVGEYH
 961 LGEFVNRFRHGSLVMRLPDSDVGQIPTVIFGTVNGVIGVIASLPHDQYLFLEKLQTNLRKVIKGVGGLSHEQWRSFYNEK
1041 KTVDAKNFLDGDLIESFLDLSRNRMEEISKAMSVPVEELMKRVEELTRLH
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